03CD

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/934,948
Source: OIPE
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OIPE

RAW SEQUENCE LISTING DATE: 08/05/2005
PATENT APPLICATION: **US/09/934,948** TIME: 16:31:26

Input Set : **A:\6229200 SEQ LISTING.ST25.txt**
Output Set: **N:\CRF4\08052005\I934948.raw**

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  3 <110> APPLICANT: Novo Nordisk A/S
  4       Schering Aktiengesellschaft
  5       Grondahl, Christian
  6       Vissing, Henrik
  7       Wahl, Philip
  9 <120> TITLE OF INVENTION: Receptors and Signalling Proteins Capabale of Binding
Meiotic
 10       Acting Sterols
 12 <130> FILE REFERENCE: 6229.200-US
 14 <140> CURRENT APPLICATION NUMBER: US 09/934,948
 15 <141> CURRENT FILING DATE: 2001-08-22
 17 <150> PRIOR APPLICATION NUMBER: US 60/231,948
 18 <151> PRIOR FILING DATE: 2000-09-09
 20 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01259
 21 <151> PRIOR FILING DATE: 2000-08-25
 23 <160> NUMBER OF SEQ ID NOS: 14
 25 <170> SOFTWARE: PatentIn version 3.3
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 28 <211> LENGTH: 2814
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Mus musculus
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 37 gctctcctac tacacgtcca aggacaaaat gatgagaggc tctcgaagag gatgcgttag    180
 39 actcagagga gctgtgattg gtatagacga cgaggacgac agcaccttca caatcactgt    240
 41 cgatcagaaa accttccact tccaggctcg agatgcagac gagcgagaga agtggatcca    300
 43 tgccttagaa gaaactattc ttcgccatac tcttcagctt caaggtttgg attcaggatt    360
 45 catccccagt gtccaagact ttgataagaa acttaccgag gctgacgcgt acctgcagat    420
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 57 agctaccttg ggacatcatc agactccaac accaaatagt acaggcagtg ggaactcacc    780
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83 ttcagccttt tatgctgagt gttttaacaa gaagatacaa ttcaatgctc atatctggac 1560
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87 gtgtctggag tacgatgagc actacatcct cacgttcccc aatggctatg gaaggtctat 1680
89 cctgacagtg ccctgggtgg aattgggagg agaatgcaat atcaactgct ccaaaacggg 1740
91 ttacagcgca aacatcgtct tccacactaa gcctttctat gggggcaaga agcacagaat 1800
93 tactgcagag atttttttctc cgaatgacaa gaaatccttc tgctcaattg aaggggaatg 1860
95 gaatggtatc atgtatgcaa aatacgcaac aggggaaaac actgtctttg tagacaccaa 1920
97 gaaattgcct ataatcaaga aaaaggtgag gaagttggaa gatcagaatg agtatgagtc 1980
99 ccgcagcctt tggaaggatg tcactttcaa tttaaaaatc agagacattg atgcagcaac 2040
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103 ggaaattcag tgggagacga ggctctttca cgaggatggc gaatgctggg tttacgatga 2160
105 gcctttactg aagcgtcttg gtgctgtgaa gcattaggcc gacaaccgag tccacacctg 2220
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117 gggcataaaa tctttatctc cagttcatat aatcttgagt tttagataka cacacatgcg 2580
119 taacagctga cagtttttca caagtacacc cacctgtaaa tactgtakcc tcagtttaga 2640
121 aaattagtgc atgtatgaaa atcaagtgtt aggaaatttc atggtttcac ctataacctt 2700
123 tattttagaa ttgaactatg attagattgt atctaaacct gaagtataat tatatgcagt 2760
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130 <212> TYPE: PRT
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140 20 25 30
143 Leu Ser Tyr Tyr Thr Ser Lys Asp Lys Met Met Arg Gly Ser Arg Arg
144 35 40 45
147 Gly Cys Val Arg Leu Arg Gly Ala Val Ile Gly Ile Asp Asp Glu Asp
148 50 55 60
151 Asp Ser Thr Phe Thr Ile Thr Val Asp Gln Lys Thr Phe His Phe Gln
152 65 70 75 80
155 Ala Arg Asp Ala Asp Glu Arg Glu Lys Trp Ile His Ala Leu Glu Glu
156 85 90 95
159 Thr Ile Leu Arg His Thr Leu Gln Leu Gln Gly Leu Asp Ser Gly Phe
160 100 105 110
163 Ile Pro Ser Val Gln Asp Phe Asp Lys Lys Leu Thr Glu Ala Asp Ala
164 115 120 125
167 Tyr Leu Gln Ile Leu Ile Glu Gln Leu Lys Leu Phe Asp Asp Lys Leu
168 130 135 140
171 Gln Asn Cys Lys Asp Asp Glu Gln Arg Lys Lys Val Glu Thr Leu Lys

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179 Leu Gln Ile Ala Lys Ser Thr Ile Asn Pro Val Asp Ala Ile Tyr Gln
180             180                 185                 190
183 Pro Ser Pro Leu Glu Pro Val Ile Ser Thr Met Pro Ser Gln Thr Ala
184         195                 200                 205
187 Leu Pro Pro Glu Pro Ala Gln Leu Cys Lys Ser Glu Gln Arg Pro Ser
188     210                 215                 220
191 Ser Leu Pro Val Gly Pro Val Leu Ala Thr Leu Gly His His Gln Thr
192 225                 230                 235                 240
195 Pro Thr Pro Asn Ser Thr Gly Ser Gly Asn Ser Pro Pro Ser Ser Ser
196                 245                 250                 255
199 Leu Thr Pro Pro Ser His Val Asn Leu Ser Pro Asn Thr Val Pro Glu
200             260                 265                 270
203 Phe Ser Tyr Ser Ser Ser Glu Asp Glu Phe Tyr Asp Ala Asp Glu Phe
204         275                 280                 285
207 His Gln Ser Gly Ser Ser Pro Lys Arg Leu Ile Asp Ser Ser Gly Ser
208     290                 295                 300
211 Ala Ser Val Leu Thr His Ser Ser Ser Gly Asn Ser Leu Lys Arg Pro
212 305                 310                 315                 320
215 Asp Thr Thr Glu Ser Leu Asn Ser Ser Met Ser Asn Gly Thr Ser Asp
216                 325                 330                 335
219 Ala Asp Leu Phe Asp Ser His Asp Asp Arg Asp Asp Asp Gly Glu Ala
220             340                 345                 350
223 Gly Ser Val Glu Glu His Lys Ser Val Ile Met His Leu Leu Ser Gln
224         355                 360                 365
227 Val Arg Leu Gly Met Asp Leu Thr Lys Val Val Leu Pro Thr Phe Ile
228     370                 375                 380
231 Leu Glu Arg Arg Ser Leu Leu Glu Met Tyr Ala Asp Phe Phe Ala His
232 385                 390                 395                 400
235 Pro Asp Leu Phe Val Ser Ile Ser Asp Gln Lys Asp Pro Arg Asp Arg
236                 405                 410                 415
239 Met Val Gln Val Val Lys Trp Tyr Leu Ser Ala Phe His Ala Gly Arg
240             420                 425                 430
243 Arg Gly Ser Val Ala Lys Lys Pro Tyr Asn Pro Ile Leu Gly Glu Ile
244         435                 440                 445
247 Phe Gln Cys His Trp Thr Leu Pro Asn Asp Thr Glu Glu Asn Ala Glu
248     450                 455                 460
251 Leu Val Ser Glu Gly Pro Val Pro Trp Val Ser Lys Asn Ser Val Thr
252 465                 470                 475                 480
255 Phe Val Ala Glu Gln Val Ser His His Pro Pro Ile Ser Ala Phe Tyr
256                 485                 490                 495
259 Ala Glu Cys Phe Asn Lys Lys Ile Gln Phe Asn Ala His Ile Trp Thr
260             500                 505                 510
263 Lys Ser Lys Phe Leu Gly Met Ser Ile Gly Val His Asn Ile Gly Gln
264         515                 520                 525
267 Gly Cys Val Ser Cys Leu Glu Tyr Asp Glu His Tyr Ile Leu Thr Phe
268     530                 535                 540
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275 Gly Gly Glu Cys Asn Ile Asn Cys Ser Lys Thr Gly Tyr Ser Ala Asn
276                 565                 570                 575
279 Ile Val Phe His Thr Lys Pro Phe Tyr Gly Gly Lys Lys His Arg Ile
280             580                 585                 590
283 Thr Ala Glu Ile Phe Ser Pro Asn Asp Lys Lys Ser Phe Cys Ser Ile
284         595                 600                 605
287 Glu Gly Glu Trp Asn Gly Ile Met Tyr Ala Lys Tyr Ala Thr Gly Glu
288     610                 615                 620
291 Asn Thr Val Phe Val Asp Thr Lys Lys Leu Pro Ile Ile Lys Lys Lys
292 625                 630                 635                 640
295 Val Arg Lys Leu Glu Asp Gln Asn Glu Tyr Glu Ser Arg Ser Leu Trp
296                 645                 650                 655
299 Lys Asp Val Thr Phe Asn Leu Lys Ile Arg Asp Ile Asp Ala Ala Thr
300             660                 665                 670
303 Glu Ala Lys His Arg Leu Glu Glu Arg Gln Arg Ala Glu Ala Arg Glu
304         675                 680                 685
307 Arg Lys Glu Lys Glu Ile Gln Trp Glu Thr Arg Leu Phe His Glu Asp
308     690                 695                 700
311 Gly Glu Cys Trp Val Tyr Asp Glu Pro Leu Leu Lys Arg Leu Gly Ala
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315 Val Lys His
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320 <211> LENGTH: 2534
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329 gctgacgcgt acctgcagat cttgatagaa caattaaagc tttttgatga caagcttcaa    180
331 aattgtaaag atgatgaaca gagaaagaaa gttgaaactc tcaaagacac aacaaatagc    240
333 atggtagaat caattaaaca ctgcattgtg ttgctacaga ttgctaaaag tactattaat    300
335 cctgtagatg caatatacca gcctagtccc ttggaacctg tgatcagcac aatgccttcc    360
337 cagactgcct tacctccaga acccgctcag ttgtgtaagt cagagcagcg tccatcttcc    420
339 ttacctgttg gacctgtgtt agctaccttg ggacatcatc agactccaac accaaatagt    480
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343 tctccaaata cagtcccaga gttctcttac tctagcagtg aagatgagtt ctatgatgct    600
345 gatgaattcc atcaaagtgg ctcgtcccca aagcgcttaa tagattcttc tggatctgcc    660
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353 ttatcacaag tcaggctggg gatggacctc acaaaggtag ttcttccaac gtttattctc    900
355 gagagaagat ctctgttaga aatgtatgca gacttttttcg cacatccaga cctgttcgtg    960
357 agcattagtg atcagaagga tcccagggat cgaatggttc aggttgtgaa atggtacctc   1020
359 tcggccttcc atgcaggaag gagaggatcg gtggccaaaa agccgtacaa tcctattttg   1080
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363 gtttcagaag ggccggttcc ctgggtttct aagaacagtg taacatttgt ggctgagcaa   1200
365 gtttcccacc atccgcccat ttcagccttt tatgctgagt gttttaacaa gaagatacaa   1260
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371 aatggctatg gaaggtctat cctgacagtg ccctgggtgg aattgggagg agaatgcaat   1440
373 atcaactgct ccaaaacggg ttacagcgca aacatcgtct tccacactaa gcctttctat   1500
375 gggggcaaga agcacagaat tactgcagag atttttctc cgaatgacaa gaaatccttc   1560
377 tgctcaattg aaggggaatg gaatggtatc atgtatgcaa aatacgcaac aggggaaaac   1620
379 actgtctttg tagacaccaa gaaattgcct ataatcaaga aaaaggtgag gaagttggaa   1680
381 gatcagaatg agtatgagtc ccgcagcctt tggaaggatg tcactttcaa tttaaaaatc   1740
383 agagacattg atgcagcaac ggaagcaaag cacagacttg aagaaagaca aagagcagaa   1800
385 gcccgagaaa ggaaggagaa ggaaattcag tgggagacga ggctctttca cgaggatggc   1860
387 gaatgctggg tttacgatga gcctttactg aagcgtcttg gtgctgtgaa gcattaggcc   1920
389 gacaaccgag tccacacctg gtgaccaggg cagtaggcgt aattaagcaa caatcgatct   1980
391 tccttcagga gagcttgtca cttccttctt aacgcagtgg ttcctatctc agggatactg   2040
393 gacttgacga cacagatgaa caattaaagt ggaaaccgct tccctttttct cctctgtggc   2100
395 agttacaatt ttgacttcag gcctgagaaa aacttcaggt ttcgaaacat gacatctctt   2160
397 ccttttccag atcccatgct ttgaaaaata tttatagaca gttccaggtc tcagcttcct   2220
399 gtcctctagt tctgctgttc gggcataaaa tctttatctc cagttcatat aatcttgagt   2280
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403 tactgtakcc tcagtttaga aaattagtgc atgtatgaaa atcaagtgtt aggaaatttc   2400
405 atggtttcac ctataacctt tattttagaa ttgaactatg attagattgt atctaaacct   2460
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417 <400> SEQUENCE: 4
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428         35                  40                  45
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432     50                  55                  60
435 Thr Thr Asn Ser Met Val Glu Ser Ile Lys His Cys Ile Val Leu Leu
436 65                  70                  75                  80
439 Gln Ile Ala Lys Ser Thr Ile Asn Pro Val Asp Ala Ile Tyr Gln Pro
440                 85                  90                  95
443 Ser Pro Leu Glu Pro Val Ile Ser Thr Met Pro Ser Gln Thr Ala Leu
444             100                 105                 110
447 Pro Pro Glu Pro Ala Gln Leu Cys Lys Ser Glu Gln Arg Pro Ser Ser
448         115                 120                 125
451 Leu Pro Val Gly Pro Val Leu Ala Thr Leu Gly His His Gln Thr Pro
452     130                 135                 140
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456 145                 150                 155                 160
459 Thr Pro Pro Ser His Val Asn Leu Ser Pro Asn Thr Val Pro Glu Phe
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13,14

VERIFICATION SUMMARY DATE: 08/05/2005
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